

1 GGAAGGTTTAAAGAAAGCCGCAAGCGCAGGAAGCCCTCCCGGCACGGGTGGGGAAAGCGGCCGTGCAGCGCGGGACAGGCACTCGGCTGGCACTGGCTGTAGGATGTCGT
M S S

-31

121 COTGATAAGGTGGGATGGACCGGCCCTCTGGGGCTTCTGCTGGCTGGTGTGGGCTTCTGGAGGCCCGCTTTCGCCCTCTCCACGTCTGCAAAATGCAGTGCTCTCGGA
-28 W I R W H G P A M A R L W G F C W L V V G F W R A A F A C P T S C K C S A S R I
+1

241 TCTGGTGACGACCCCTTCTCTGGCATCGTGGCATTTCCGAGATTGGAGCTAACAGTGTAGATCCTGAGACATCACCGAAATTTTCATCGCAACACGAGAAAAGGTTAGAAATCATCA
13 W C S D P S P G I V A F P R L E P N S V D P E N I T E I F I A N Q K R L E I I N

361 AGAAGATGATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAAATGTGGATCTGGATTAATAATTTGTGGCTCATAAAGCATTTCTGAAAAACAGCAACCTGCAGCACATCAATTTTA
53 E D D V E A Y V G L R N L T I V D S G L K F V A H K A F L K N S N L Q H I N F T

481 CCGAAACAAACTGACGAGTTTGTCTAGGAAACATTTCCGTACCTTGACTTGTCTGAATGATCCTCGTGGGCAATCCATTTACATGCTCCTGTGACATTTATGTGATCAAGACTCTCC
93 R N K L T S L S R K H F R H L D L S E L I L V G N P F T C S C D I M W I K T L Q

601 AAGAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCCCTGAATGAAGCAAGAAATATTCCCTGGCAACCTGCAGATACCCAAATTTGTGGTTTGCATCTGCAAAATCTGGCCG
133 E A K S S P D T Q D L Y C L N E S S K N I P L A N L Q I P N C G L P S A N L A A

721 CACCTAACCTCACTGTGAGGAAGGAAAGTCTATCACATTTATCTGTAGTGTGGCAGGTGATCCGGTTCCCTAATATATGTTGGGATGTTGTPAACCTGGTTTCCAAACATATGAATGAAA
173 P N L T V E E G K S I T L S C S V A G D P V P N M Y W D V G N L V S K H M N E T

841 CAAGCCACACAGGGCTCCTTAAGATAACTAAACATTTTCATCCGATCAGTGGGAAGCAGATCTCTGTGTGGGAAAAATCTGTAGGAAGAATCAAGATTTCTGCAACCTCACTG
213 S H T Q G S L R I T N I S S D D S G K Q I S C V A E N L V G E D Q D S V N L T V

961 TGCATTTGCAACCACTATCACATTTCTCGAATCTCCAACTCAGACCACCTGCTGCAATCCATTCATCTGTGAAGCAACCCAAACCCAGCGCTTCAGTGGTCTATATAACGGGCAA
253 H F A P T I T F L E S P T S D H H W C I P F T V K G N P K P A L Q W F Y N G A I

1081 TATTGAATGAGTCCAAATACATCTGTACTAAATACATGTTACCAATCACACGGAGTACCACGGCTGCCCTCCAGCTGGATAATCCCACTCACATGAACAATGGGGACTACACTCTAATAG
293 L N E S K Y I C T K I H V T N H T E Y H G C L Q L D N P T H M N N G D Y T L I A

1201 CCAAGATGAGTATGGGAAGGATGAGAAACAGATTTCTGCTCACTTCAATGGCTGGCTGGAATTCACGATGGTGCACCCAAATTCCTGATGTAATTTATGAAGATTATGGAACCTG
333 K N E Y G K D E K Q I S A H F M G W P G I D D G A N P N Y P D V I Y E D Y G T A

1321 CAGCGAATGACATCGGGGACACCACGAACAGTAATGAATCCCTTCCACAGACGTCACATGATAAAAAACGGTCCGGAAACATCTCTCGGTCTATGCTGTGGTGGTGGTGGTGGTGGTGG
373 A N D I G D T T N R S N E I P S T D V T D K T G R E H L S V Y A V V I A S V Y

1441 TGGGATTTTGGCTTTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACACACTCCAAAGTTTGGCATGAAAGGCTCCAGCCCTCCGTTATCAGCAATGATGATGACTCTGCCAGCCCACTCCATC
413 G F C L L V M L F L L K L A R H S K F G M K G P A S V I S N D D S A S P L H H

1561 ACATCTCCAATGGGAGTAACACTCCATCTCTTCGGAAGGTGGCCAGATGCTGTCTATTGGAATGACCAAGATCCCTGTCTCATTTGAAATCCCACTACTTTGGCATCACCAACAGTC
453 I S N G S N T P S S S E G G P D A V I I G M T K I P V I E N P Q Y F G I T N S Q

FIG. 1A

1681 AGCTCAAGCCAGACACATTTGTTTCAGCACATCAAGCGACATAACAATTGTTCTCAAAAAGGAGACTAGCGAAGGAGCCTTGGAAAAGTGTTCTAGCTGAATGCATAAACCCTGTCTCCTG
493 L K P D T F V Q H I K R H N I V L K R E L G E G A F G K V F L A E C Y N L C P E

1801 AGCAGGACAAAGATCTTGGTGGCAGTGAAGACCCCTGAAGATGCCAGTGACAAATGACACGCAAGGACTCCACCGTAGGGCCGAGCTCCTGTGACCAACCTCCAGCATGAGCACATCGTCAAAGT
533 Q D K I L V A V K T L K D A S D N A R K D F H R E A E L T N L Q H E H I V K F

1921 TCTATGGCGTCTGCGTGGAGGGGACCCCTCATCATGGTCTTTGAGTACATGAAGCATGGGGACCTCAACAAAGTTCTCAGGGCACACGGCCCTGTGATGCCCTGTGATGGCTGAGGGCA
573 Y G V C V E G D P L I M V F E Y M K H G D L N K F L R A H G P D A V L M A E G N

2041 ACCGGCCCACGGAACGTACGCGACTCGCAGATGCTGCATATAGCCCCAGCAGATCGCGCGGGGATGGTTACCTGGCGTCCAGCAGCTTCGTGCACCGGATTTGGCCACCAGGAACCTGCC
613 P P T E L T Q S Q M L H I A Q I A A G M V Y L A S Q H F V H R D L A T R N C L

2161 TGGTCGGGGAGAACCTTGCTGTGTAATAATCGGGGACTTTGGGATGTCCCGGACGTGTACAGCACTGACTACTACAGGTCCGTGGCCACACAATGCTGCCCATTCGCTGGATGCCCTCCAG
653 V G E N L L V K I G D F G M S R D V Y S T D Y Y R V G G H T M L P I R W M P E

2281 AGAGCATCATGTACAGGAAATTCACAGCGGAAAGCAGCTCTGGAGCCTGGGGTCTGTGTGGAGATTTTCACTATGGCAAACAGCCCTGGTACCAGCTGTCAAACAATGAGGTGA
693 S I M Y R K F T T E S D V W S L G V V L W E I F T Y G K Q P W Y Q L S N N E V I

2401 TAGAGTGTATCACTCAGGCCCAGTCTCTGCAGGACCCCGCACGTCGCCCCAGGAGGTGTATGACTGATGCTGGGTGCTGGCAGCGAGACCCACATGAGGAAGAACAATCAAGGGCA
733 E C I T Q G R V L Q R P R T C P Q E V Y E L M L G C W Q R E P H M R K N I K G I

2521 TCCATACCCTCCTTCAGAACTTGGCCAGGCATCTCCGGTCTACCTGGACATTC TAGGTAGGGCCCTTTTCCCCAGACCGATCCTTCCCAACGTACTCCTCAGACGGGCTGAGAGGATG
773 H T L L Q N L A K A S P V Y L D I L G O

2641 AACATCTTTTAACTGCCGCTGGAGGCCAACCAAGTCTCTCCTTCACTCTGACAGTATTAAACATCAAAGACTCCGAGAAAGCTCTCGAGGGAAGCAGTGTGFACCTCTTCATCATCATAGACA
2761 CAGTATTGACTTCTTTTGGCATTTATCTCTCTCTCTCTCCATCTCCCTTGGTGTTCCTTTTCTTTTTTAAAAATTTTCTTTTTTTCGTTCTCCCTGCTTCCAGTATTC

2881 TTACCCCTTTCTTTTGAATCAATCTGGCTTCTGCAATTAATACTCTGCATAGACAAAGGCCTTAACAAAACGPAATTTGTTATATACGACAGACACTCCAGTTTGCCCAACCAACTAAAC
3001 AATGCCTTGTATTCTCCTGCCCTTTGATGTGGATGAAAAAAGGGAAAAACAAATATTTCACTTAAACCTTGTCACTCTGCTGTACAGATATCGAGAGTTTCTATGGATTCACTTCTTATTT

3121 TATTTATATTATTAATCTGTTCTTATTTGATGGCTTAAGCCTGTGTATAAAAAAATAATCTAGA

FIG. 1B

1511 TTTTGTGTTTTCATAAGATCCCACTGGATGGTAGCTGAAATAAAGGAAAAGACAGAGAAAGGGCTGTGCTGTGTTGTTGATGCTGCCATGTAAGCTGGACTCTCTGGACTGCT
 436 F V L F H K I P L D G O
 1631 GTTGGCTTATCCCGGGAAGTGTGCTTATCTGGGGTTTTCTGTGTAGATGTGGCGGTGTTTGGAGGCTGTACTATATGAAGCCTGCATATACTGTGAGCTGTGATTGGGGAACACCAATG
 1751 CAGAGGTAACCTCAGGCAGCTAAGCAGCACCTCAAGAAACATGTTAAATTAATGCTTCTCTCTTACAGTAGTTCAAAATACAAAACCTGAAATGAAATCCCATTTGGATTGTACTTCTCT

FIG. 1C

1 GGATCCGGCTGGAGATGGATGTCTCTTTGCCAGCCAAAGTGTAGTTTCTGGCGGAATTTTCTTGGTGGGAAGCGTCTGGCTGTGGCTCGTGTGGCTTGGCCCTGCAAAAT
M D V S L C P A K C S F W R I F L L G S V W L D Y V G S V L A C P A N +1
-31
121 TGTGTCTGAGCAAGACTGAGATCAATTCGGCGGCGCGAGATGGGAACCTCTTCCCTCTCGAAGCGCAGGATTTCAGGGAACAGCAATGGGAAGCCCAATATCAACATCACGGAC
5 C V C S K T E I N C R P D D G N L F P L L E G Q D S G N S N G N A N I N I T D
241 ATCTCAAGGAATATCACTTCCATACACATAGAGAATCGGCGAGTCTTCAACGCTCAACCGCGTGGACATGGAGCTTACACCGGACTTCAAAAGCTGACCATCAAGAATCAGGACTT
45 I S R N I T S I H I E N W R S L H T L N A V D M E L Y T G L Q K L T T I K N S G L
361 CGGAGCATTCAGCCCGAGAGCGCTTTGGCAAGAACCCCAATTTGGCTTATATAACCTGTCAAGTAACTGCTCAAGTAACTGCTCAACACTCTCTGTGGCAGCTTCTCCAGAGCTGAGTCTTCGGGAATTTG
85 R S I Q P R A F A K N P H L R Y I N L S S N R L T T L S W Q L F Q T L S L R E L
481 CAGTTGGAGCAGAACATTTTCAACTGAGCTGTGACATCGCTGTGATCGCTCTGGCAGGAGCAGGGGAGGCCAAGCTCAACAGCCAGAACCTCTACTGTCATCAATGCTGATGGCTCC
125 Q L E Q N F F N C S C D I R W M Q L W Q E Q G E A K L N S Q N L Y C I N A D G S
601 CAGCTTCTCTCTTCGCAATCACTGTCAGTGTGACCTTCTCTGAGATCAGCTGAGCGCAGTCAACCTGACCTGACGAGGGTGCAATGCTGTATTATCACTTCCAAATGGCTCTGGA
165 Q L P L F R M N I S Q C D L P E I S V S H V N L T V R E G D N A V I T C N G S G
721 TCACCCCTTCTGTGACTGGATGACTGCGCTGCTGATCGCTGTGATCGCTCTGGACCAATCTGAAGTGGACCAATGTCATGTCATCAACTGACCTGGTGAATGTGAGCAGT
205 S P L P D V D W I V T G L Q S I N T H Q T N L N W T N V H A I N L T L V N V T S
841 GAGGACAAATGGCTTCAACCTGAGTGTGAGAGAACGTTGTGGGATGAGCAATGCGCAATGCGCAGCTCTACTGTCTATCTCCCCAGCTGTGTGAGCTGGAGGACCTGAGCTG
245 E D N G F T L T C I A E N V V G M S N A S V A L T V Y Y P P R V V S L E E P E L
961 CGCTGGAGCACTGCAGTTTGTGTGGTGGCAACCCCAACGCTGCACTGGCTGCACAAATGGCAGCTCTTGGGAGTCCAAGATCATCCATGTGGAATACTACCAAGAG
285 R L E H C I E F V V R G N P P P T L H W L H N G Q P L R E S K I I H V E Y Y Q E
1081 GGAGAGATTTCGAGGCTGCTCTCTTCAACAGCCCACTACAACTAGCAATAGGCAACTATACCTCAATTCGCAAAACCCACTGGGCGCAGCCCAACAGACCATCAATGGCCACTTC
325 G E I S E G C L L F N K P T H Y N N G N Y T L I A K N P L G T A N Q T I N G H F
1201 CTCAGGAGCCCTTTCAGAGAGCAAGGATAACTTTATTTGTGACGAAGTGAATCCACACCTCTATCACTGTGACCCCAACAGCAGAGACACTTTTGGGGTATCCATAGCA
365 L K E P F P {E S T D N F I L F} D E V S P T P P I T V T H K P E E D T F G V S I A
1321 GTTGACTTGTCTTTTGCTGTCTGTGTGTCTCTCTCTGTCATGATCAACAAATATGTGACGGTCCAAATTTGGAATGAAGGTCCTGGCTGTCAATCAGTGTGTGAGGAG
405 V G L A A F A C V L L V Y L F V M I N K Y G R R S K F G M K G P V A V I S G E E
1441 GACTCAGCCAGCCACTGCACACATCAACCCAGGCATCACCGCCTGTGCTCACTGGATGCGCGGCCGACACTGTGTCTATTGGCATGACTCGCATCCCTGTCAITTGAGAACCCCGAG
445 D S A S P L H H I N H G I T T P S S L D A G P D T V V I G M T R I P V I E N P Q

FIG. 2A

1561 TACTTCGTCAGGGACACAACTGCCACAAGCCGGACACGTTATGTGCACACATTAAGAGAGGAGACATCGTCTGAAGCGAGAACTGGGTGAGGGAGCCTTTGGAAAGGTCTTCTGGGCC
485 Y F R Q G G H N C H K P D T Y V Q H I K R R D I V L K R E L G E G A F G K V F L A
1681 GAGTGTACAACCTCAGCCGACCAAGGACAAGATGCTGTGGCTGTGAAGCCCTGAAGATCCACCTCGCTGCCCGAAGGATTTCCAGAGGAGGCCGAGCTGCTCACCAACCTG
525 E C Y N L S P T K D K M L V A V K A L K D P T L A A R K D F Q R E A E L L T N L
1801 CAGCATGAGCATTGTCAAGTTCTATGGAGTGTGGCGCATGGGGACCCCTCATGTGCTTTGAATACATGAAGCATGGAGACCTGAAATAGTTCTCAGGGCCCATGGGCCAGAT
565 Q H E H I V K F Y G V C G D G D P L I M V F E Y M K H G D L N K F L R A H G P D
1921 GCAATGATCCTTGTGTGATGGACAGCCAGCCAGCGGTGAGCTGGGCTCTCCAAATGCTCCAGTCCAGTCCGCTCGGTATGGTGTACCTGGCCTCCAGCACTTT
605 A M I L V D G G Q P R Q A K G E L G L S Q M L H I A S Q I A S G M V Y L A S Q H F
2041 GTGCACCGAGACCTGGCCACAGGAACCTGCTGTGAGCGGAATCTGCTAGTGAAGATTGGGACTCGGCATGTCCAGAGATGTCTACAGCACGGATTATTACAGGCTCTTTAATCCA
645 V H R D L A T R N C L V G A N L L V K I G D F G M S R D V Y S T D Y Y R {L F N P
2161 TCTGGAATGATTTTTGTATATGGTGTGAGGTGGGAGGACACACCATGCTCCCATTCGCTGATGCTCTGAAAGCATCATGTACCGGAAGTTCACTACAGAGAGTCATGTATGGAGC
685 S G N D F C I W C E} V G G H T M L P I R W M P P E S I M Y R K F T T E S D V W S
2281 TFCGGGTGATCCTCNGGGAGATCTTACCTATGAAAGCAGCCATGTTCCAACTCTCAACACGAGGTCAATTGAGTGCATTACCCAAAGTTCGTGTTTTGAGCGGCCCGAGTCTGC
725 F G V I L W E I F T Y G K Q P W F Q L S N T E V I E C I T Q G R V L E R P R V C
2401 CCCAAAGAGGTGTACGATGTCTGCTGGGTGCTGCAGAGGGAACACAGAGGTTGAACATCAAGGAGATCTACAAATCTCCATGCTTTTGGGAAGGCCACCCCAATCTACCTG
765 P K E V Y D V M L G C W Q R E P Q Q R L N I K E I Y K I L H A L G K A T P I Y L
2521 GCAATCTTGGCTAGTGTGGTGGTGCATGAATTCATCTCTGTTGGCTCTCTCTCCCTCCATCTCCCTCCCACTCCACTCCCTTCCATCTCTGACTGAAGCGGAACATC
805 D I L G O
2641 TTCAATAAACTCAAGTGCCTGTACACATACAACACTGAAAAGGAAGAAAAAGAAAAAAGAAAAAAGCGC

FIG. 2B

1600 TGGGTCTTTTCAAACATAGACAAATCATGGGATATTAACTTGAAGGACAATAGAGATCATCTAGTCCCATCAACTCACTATATATATGAGGAACCTGAGCTCCAGAGTGGGAAGTGTCT
 498 W V F S N I D N H G I L N L K D N R D H L V P S T H Y I Y E P E V Q S G E V S
 1720 TACCCAAAGGTCACATGGTTTCAGAGAAATATGTTGAATCCCAATAGCCTTCCCGGACATTCCAAGCCTCTTAAACCATGGCATCTATGTTGAGGATGTCAATGTTTATTTTCAGCAAGGA
 538 Y P R S H G F R E I M L N P I S L P G H S K P L N H G I Y V E D V N V Y F S K G
 1840 CGTCATGGCTTTTAAAC
 578 R H G F O

FIG. 2C

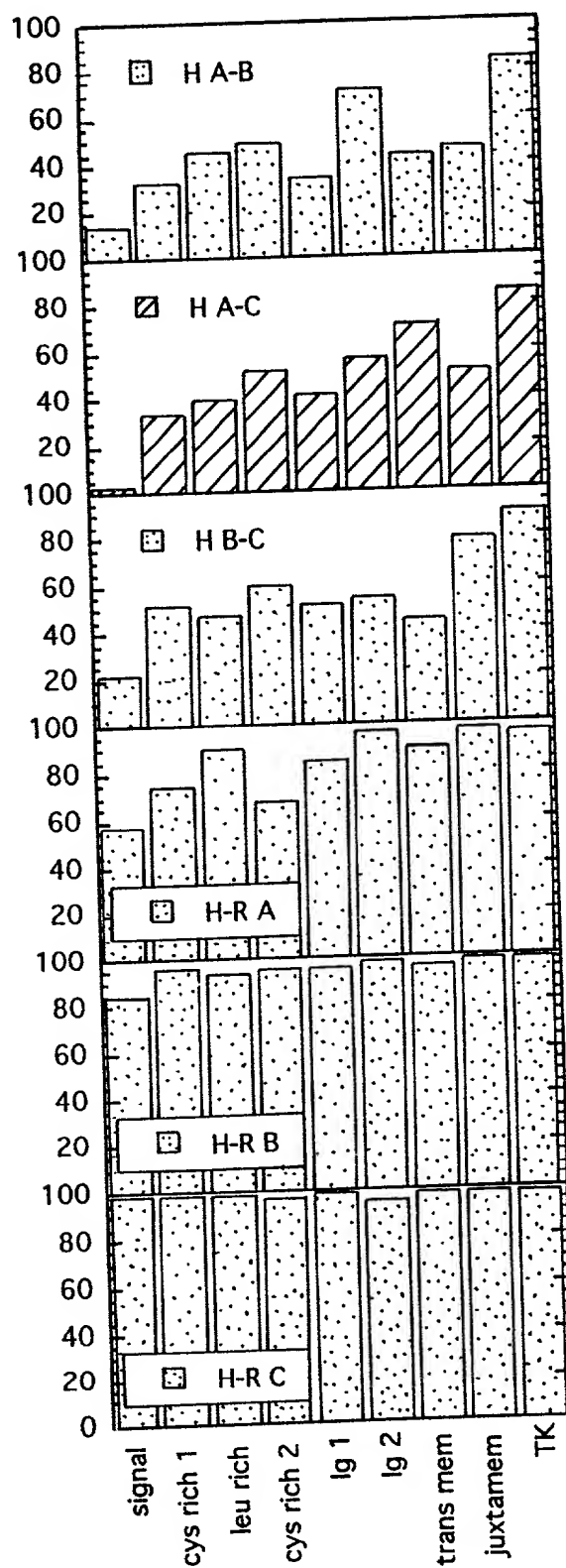


FIG. 3

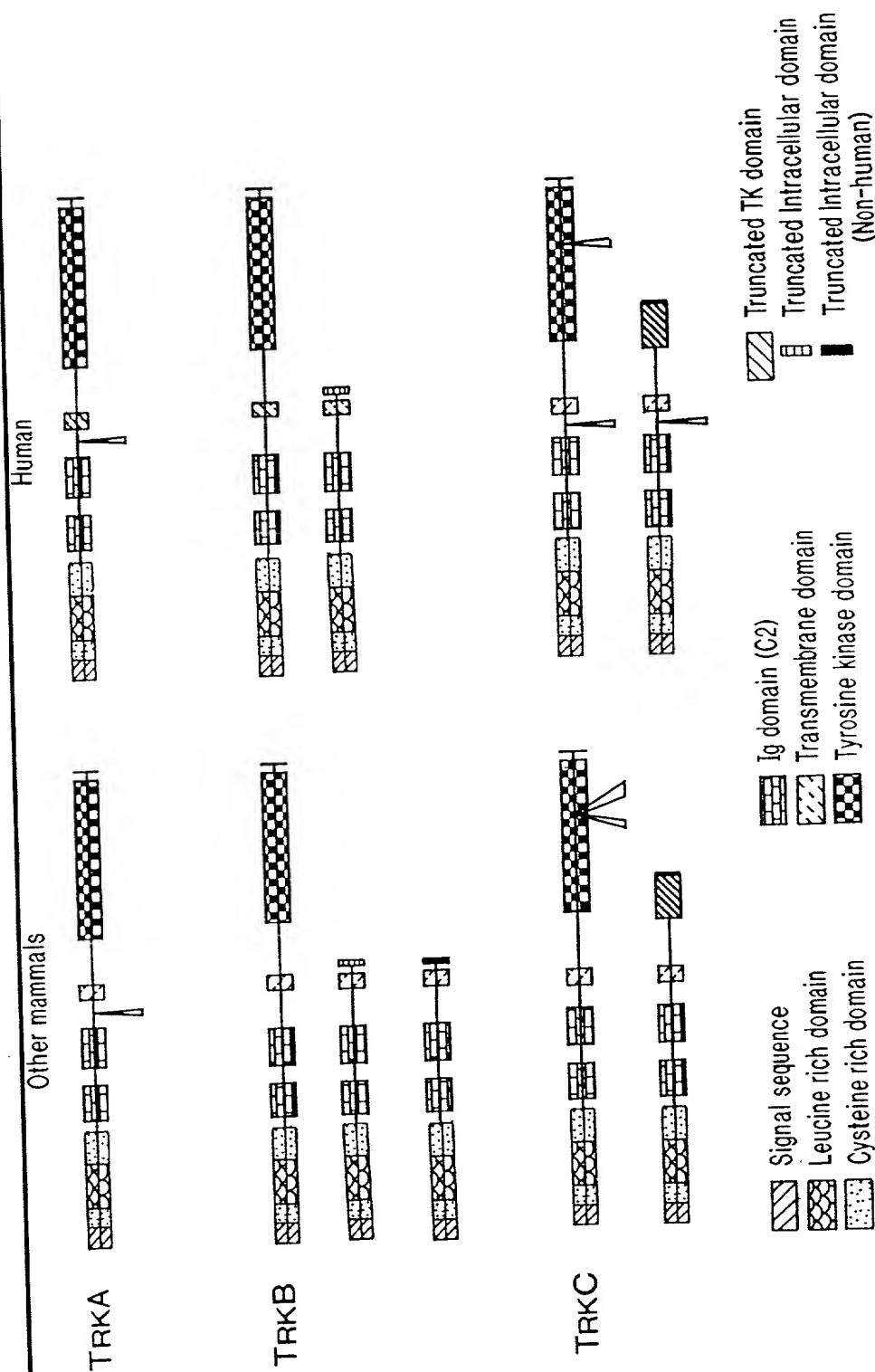


FIG. 4

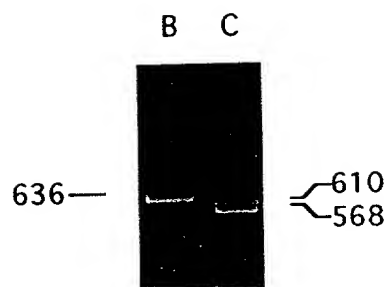


FIG. 5

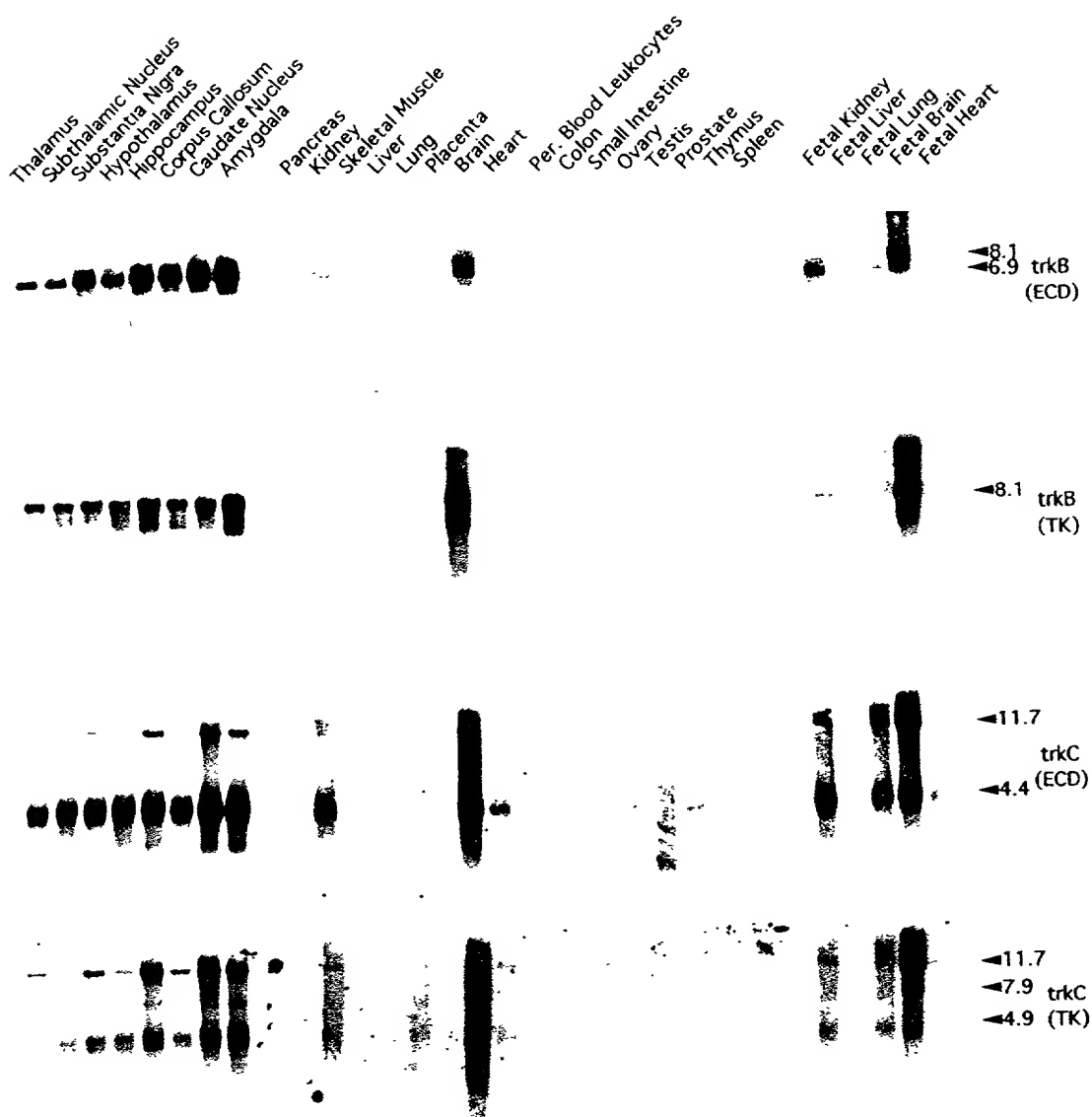


FIG. 6

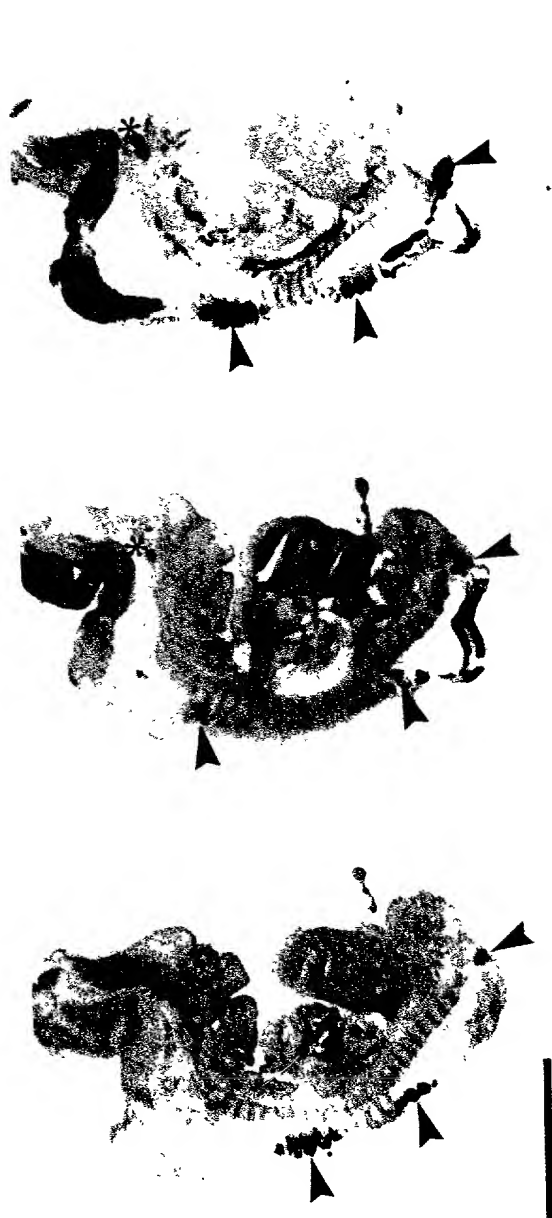


FIG. 7A

FIG. 7B

FIG. 7C



FIG. 7D



FIG. 7E



FIG. 8A

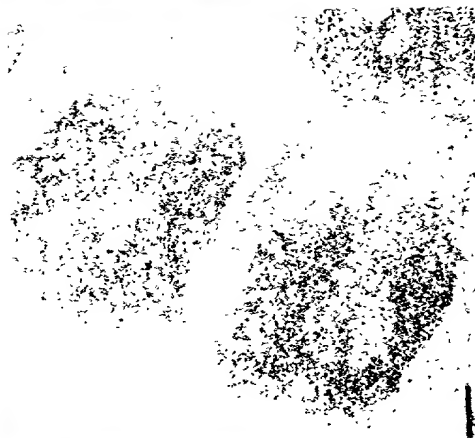


FIG. 8B

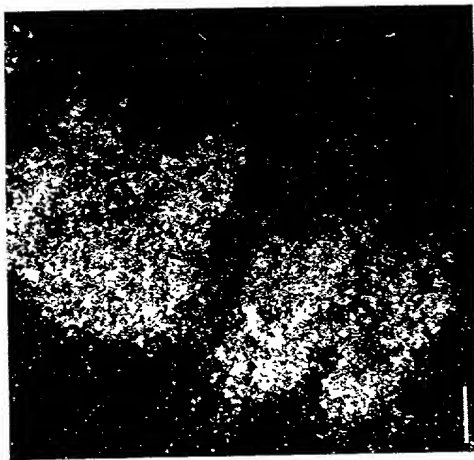


FIG. 8C

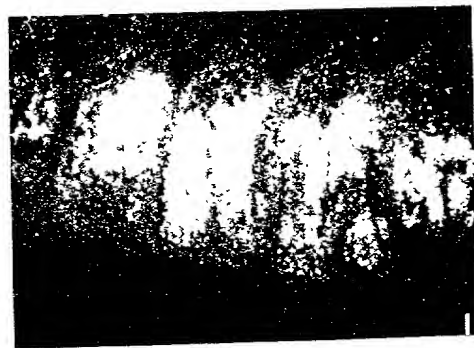


FIG. 8D



FIG. 8E

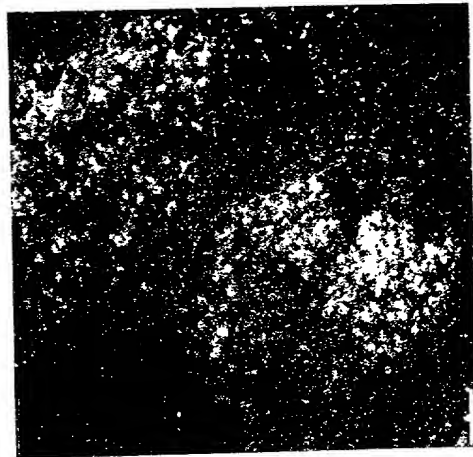


FIG. 8F

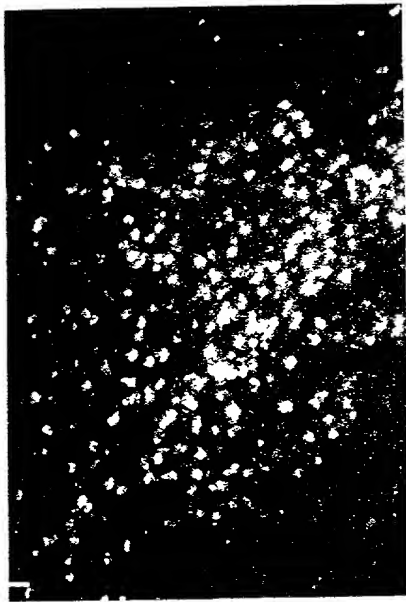


FIG. 9A



FIG. 9B

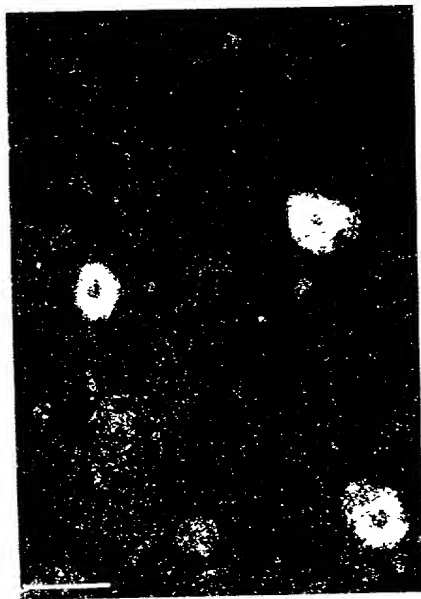


FIG. 9C



FIG. 9D

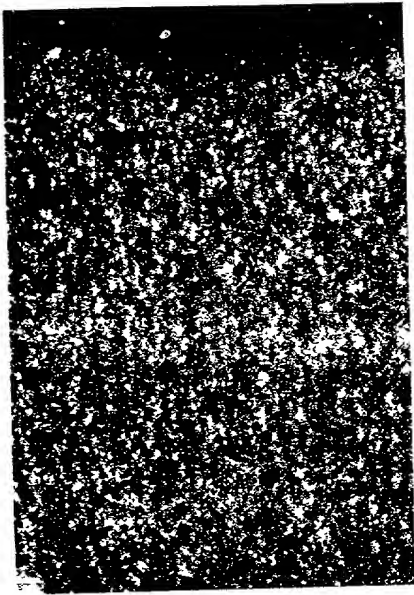


FIG. 9E

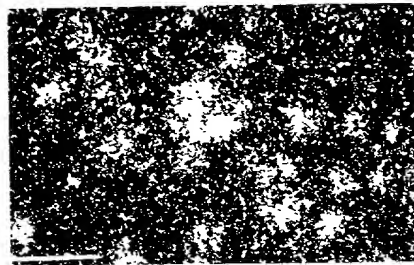
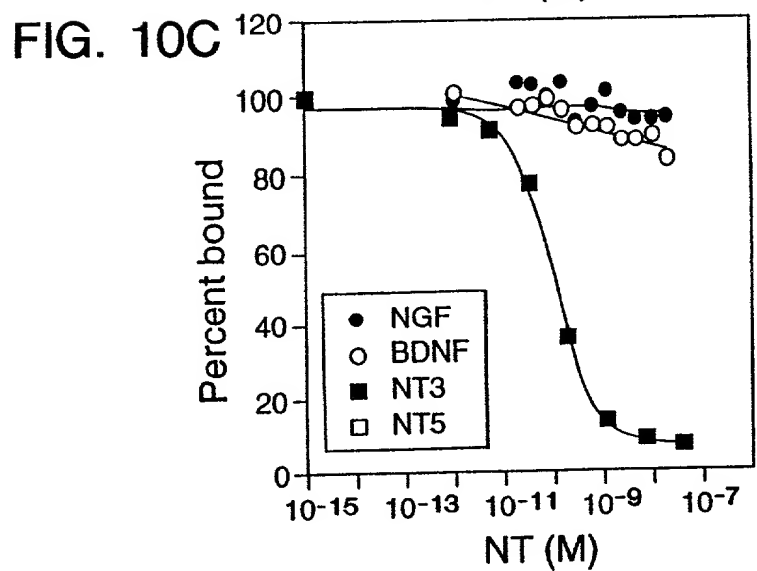
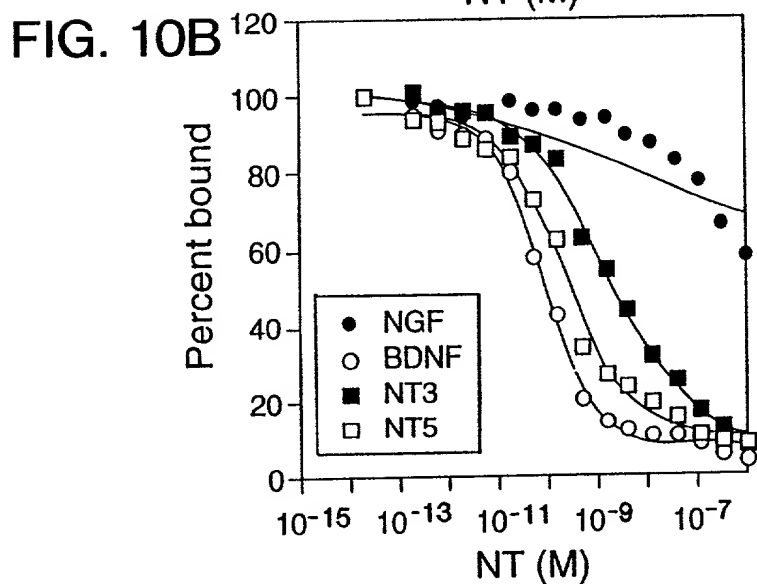
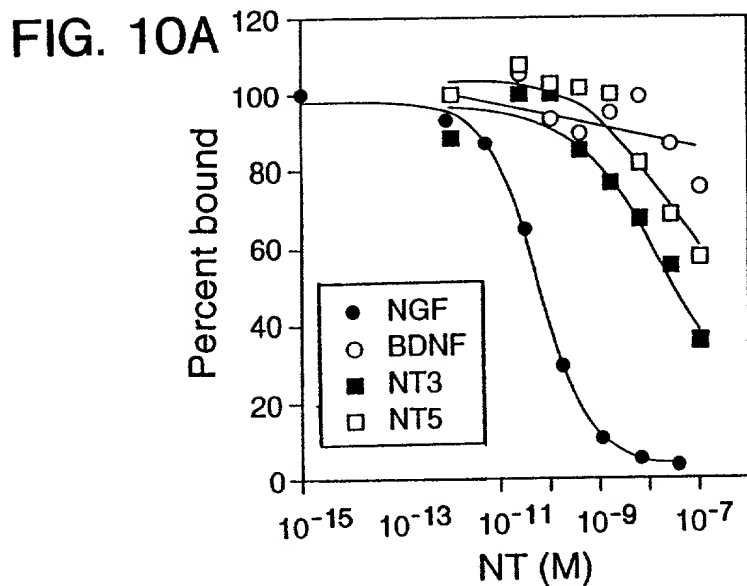
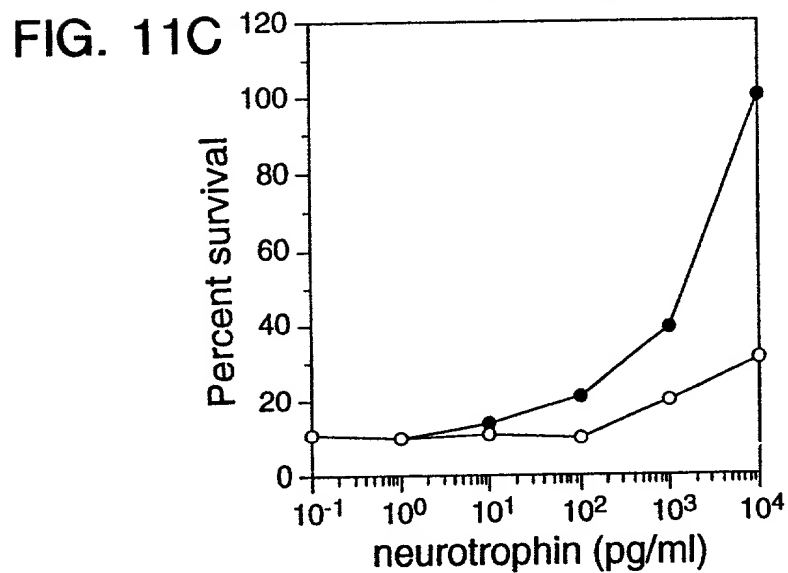
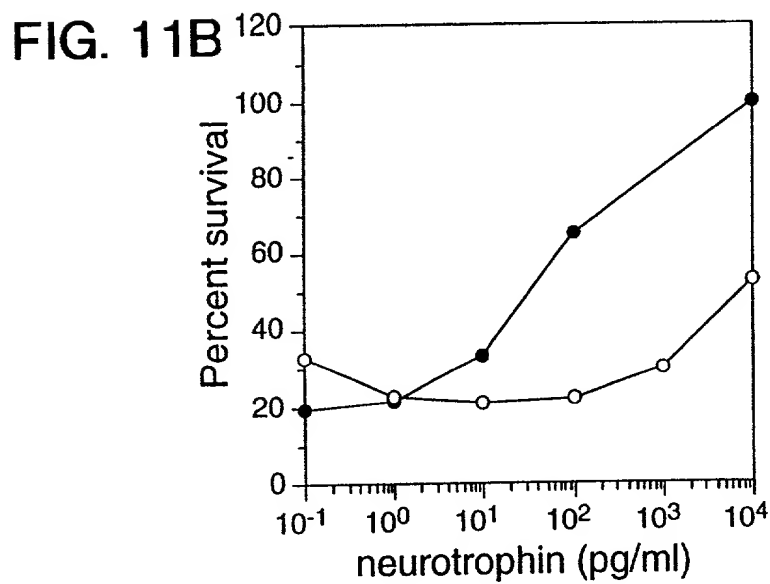
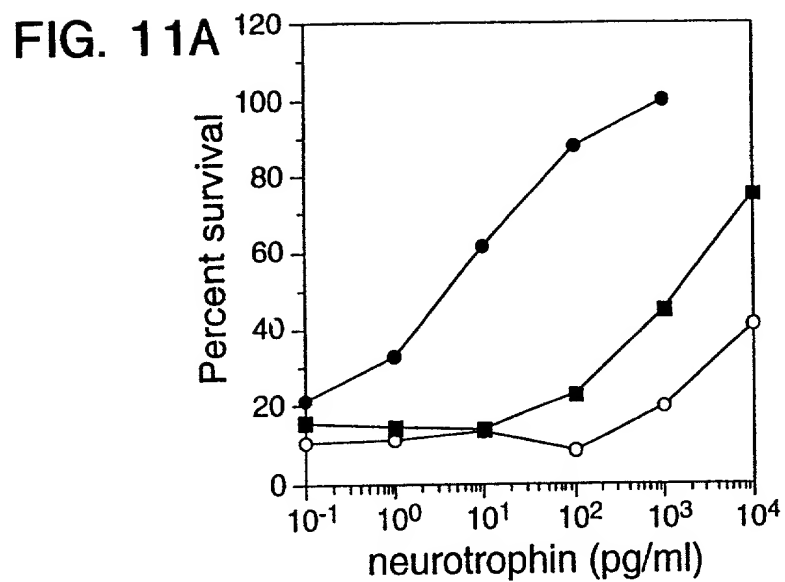


FIG. 9G

FIG. 9F



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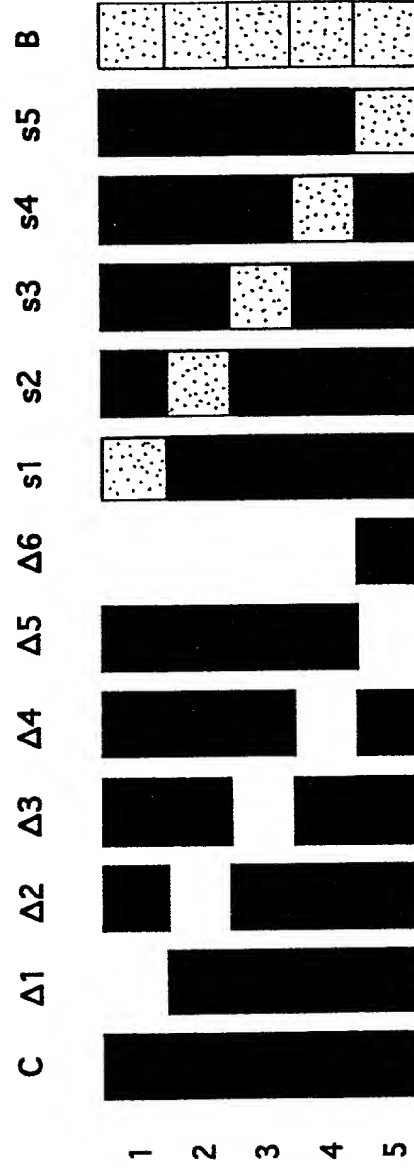


FIG. 12

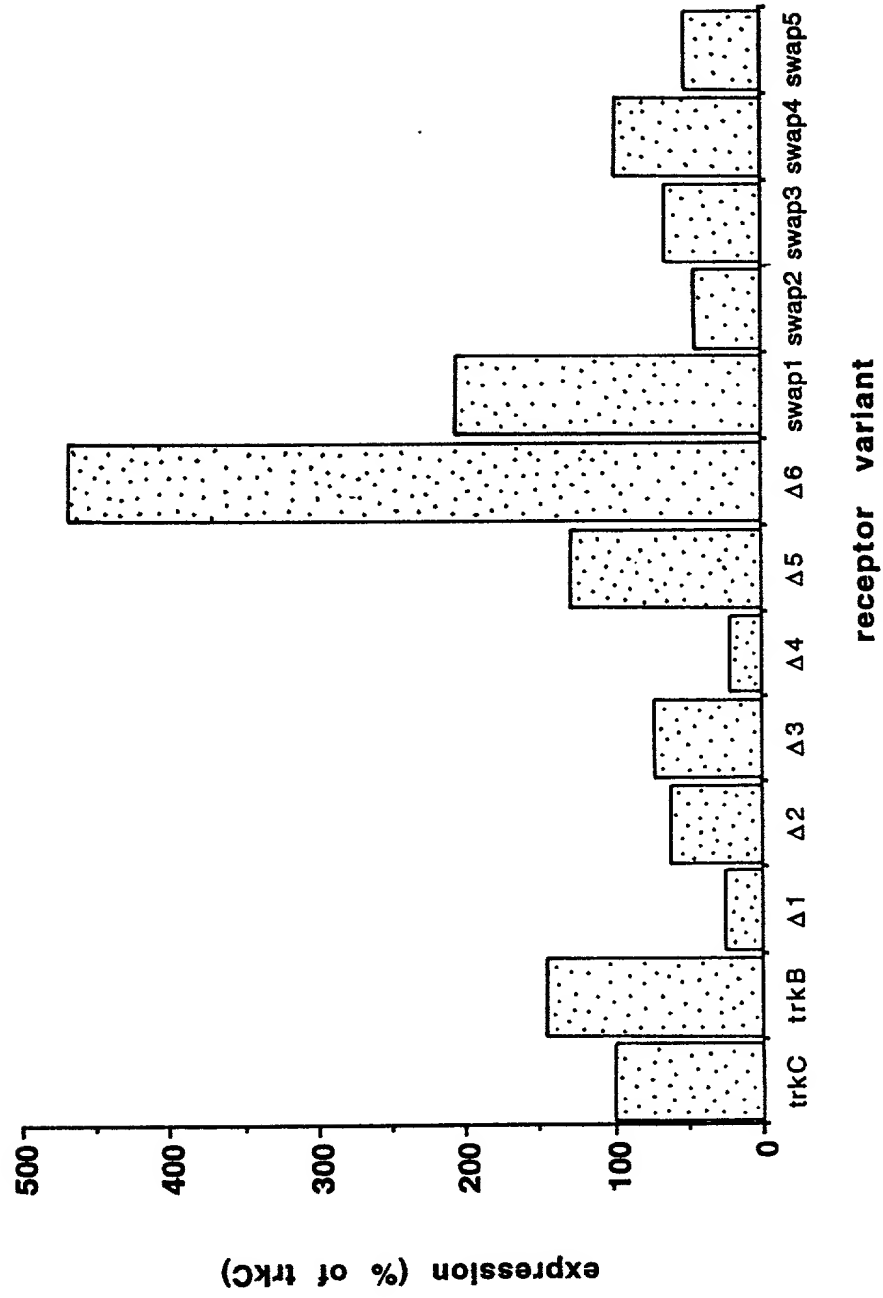


FIG. 13

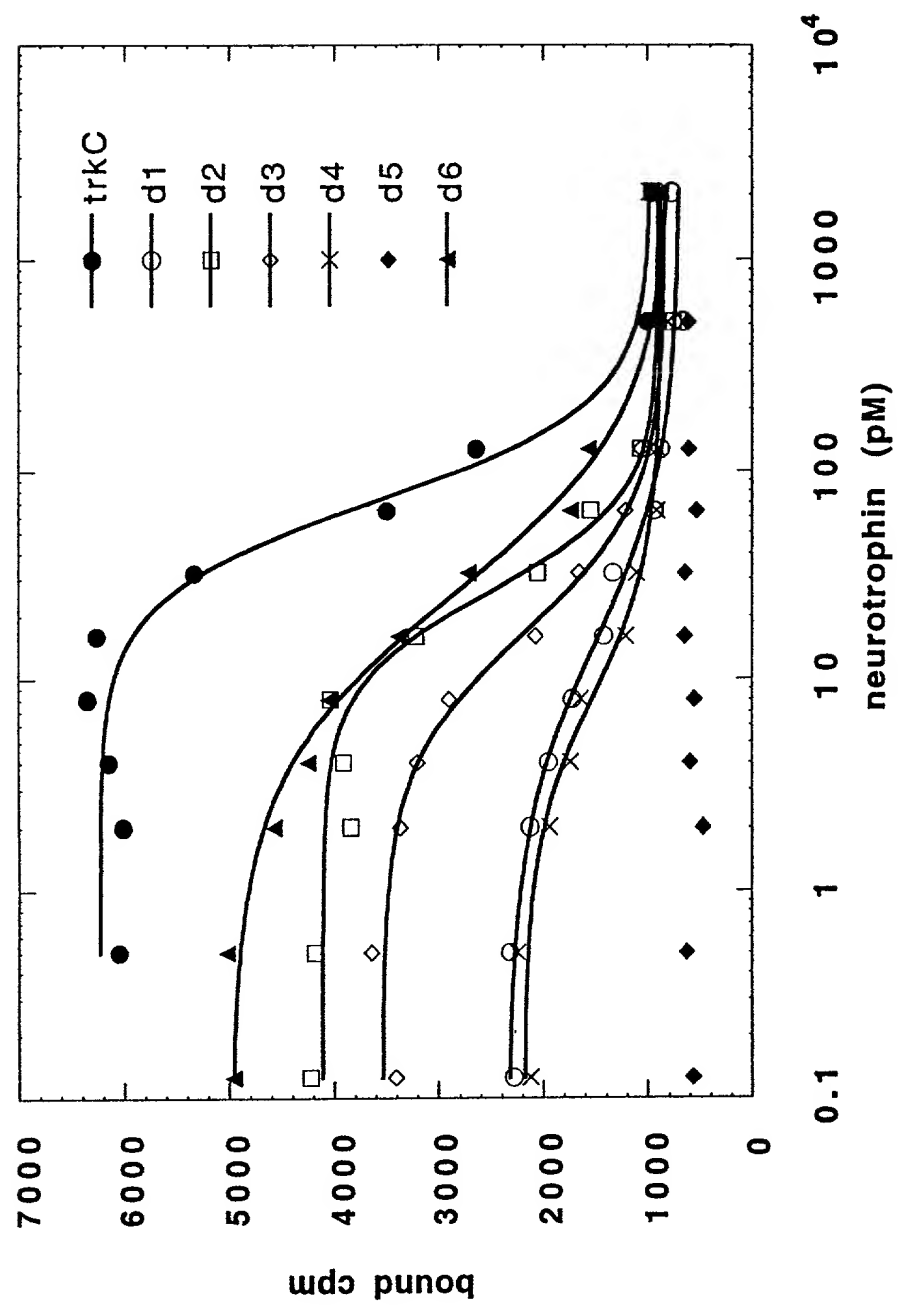


FIG. 14A

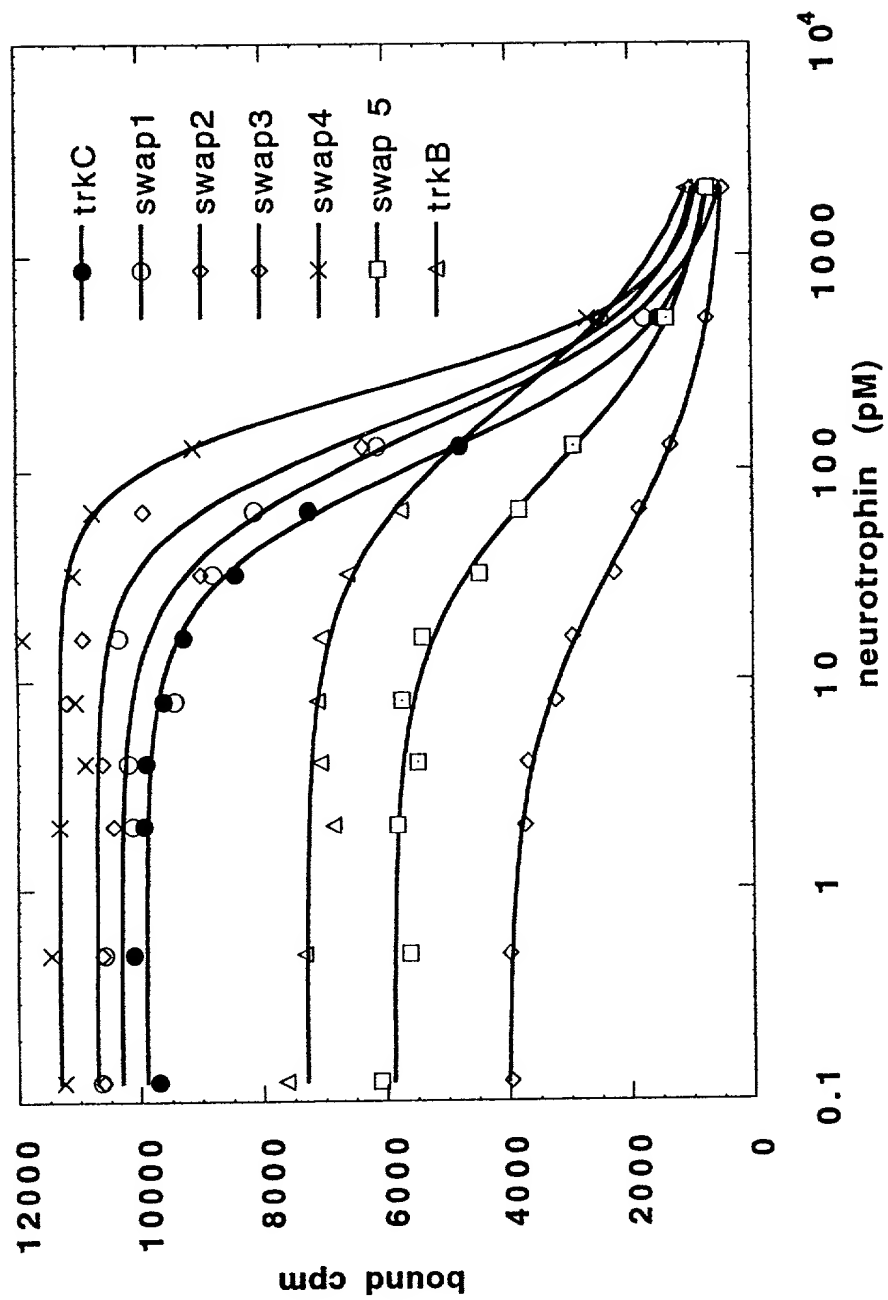


FIG. 14B

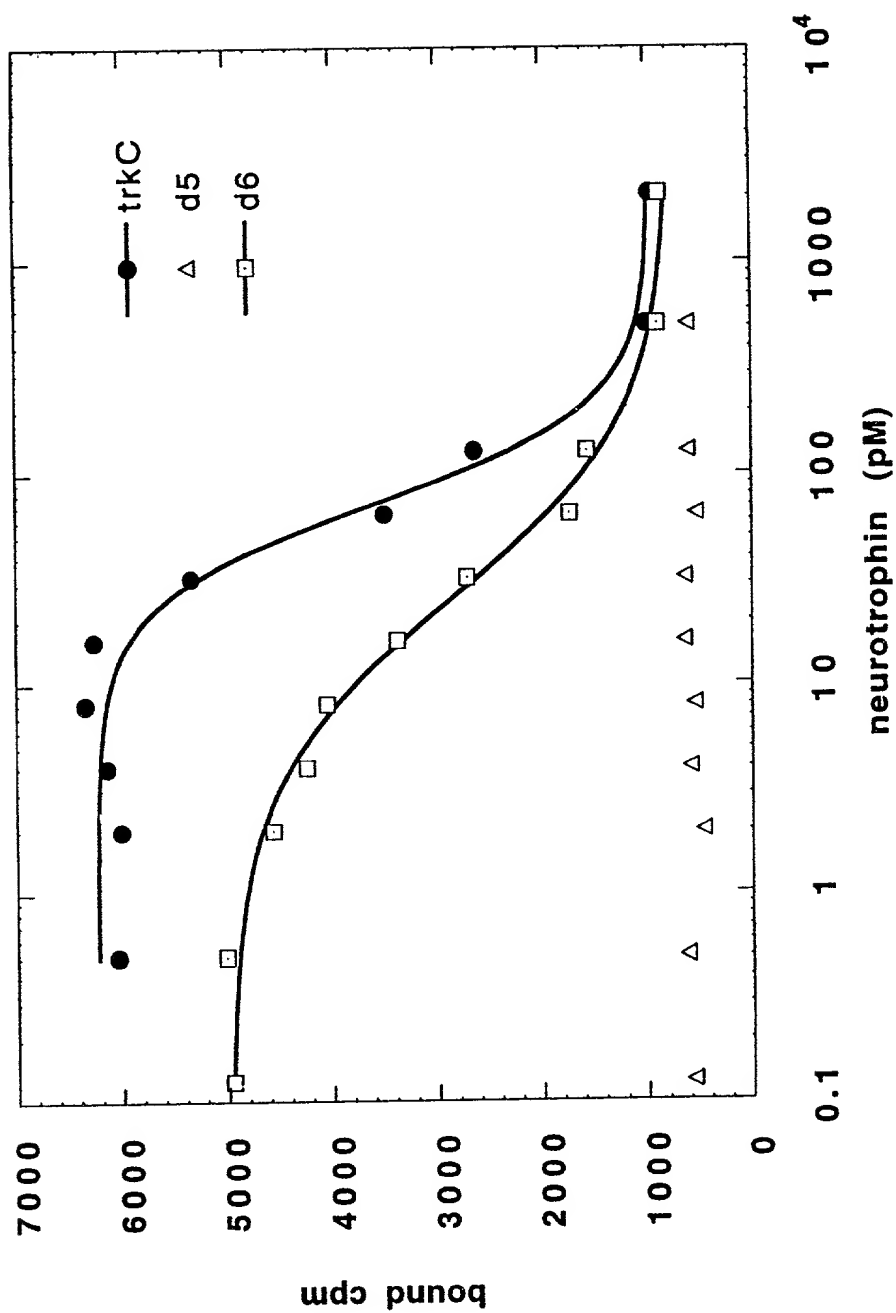


FIG. 14C

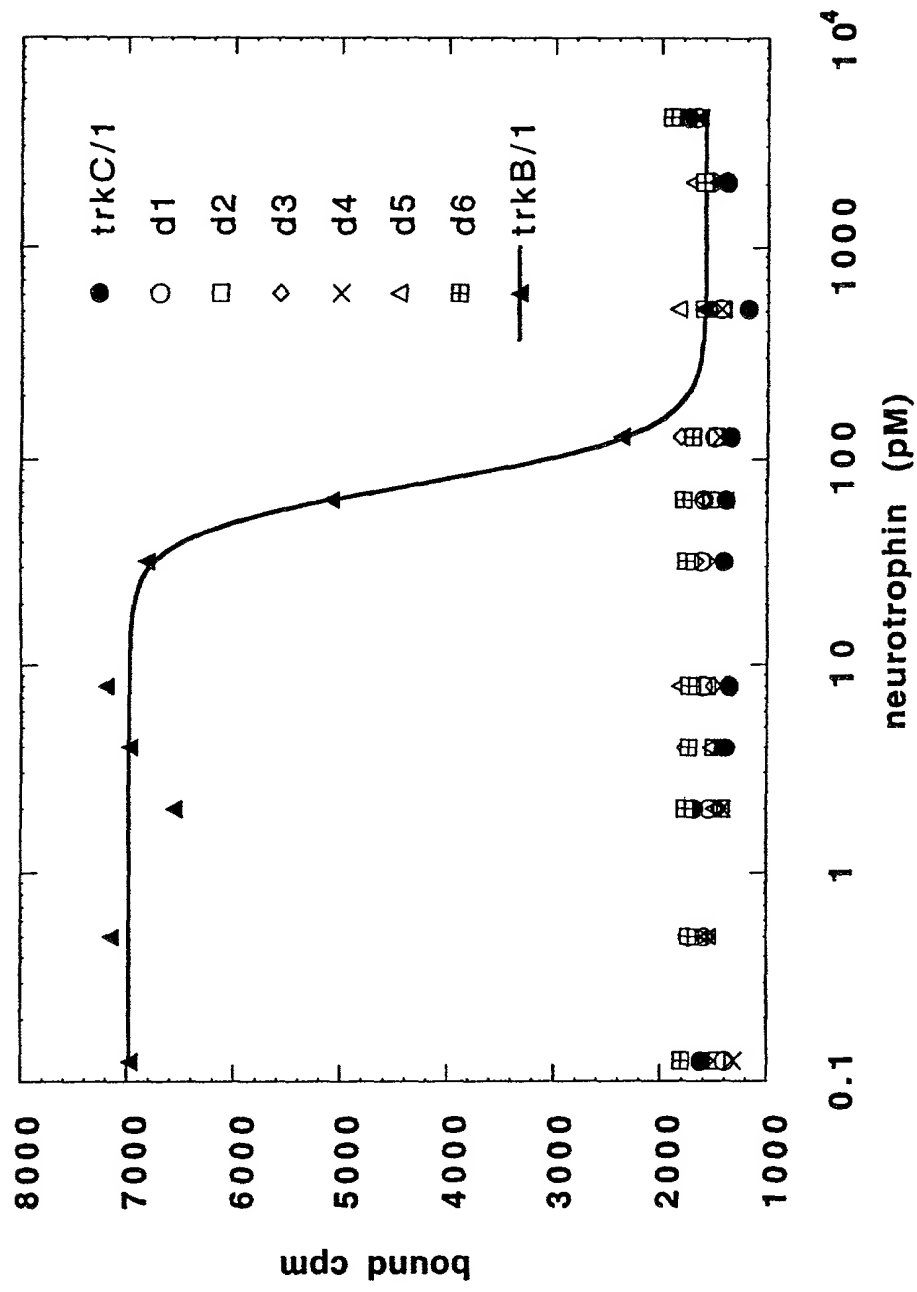


FIG. 15A

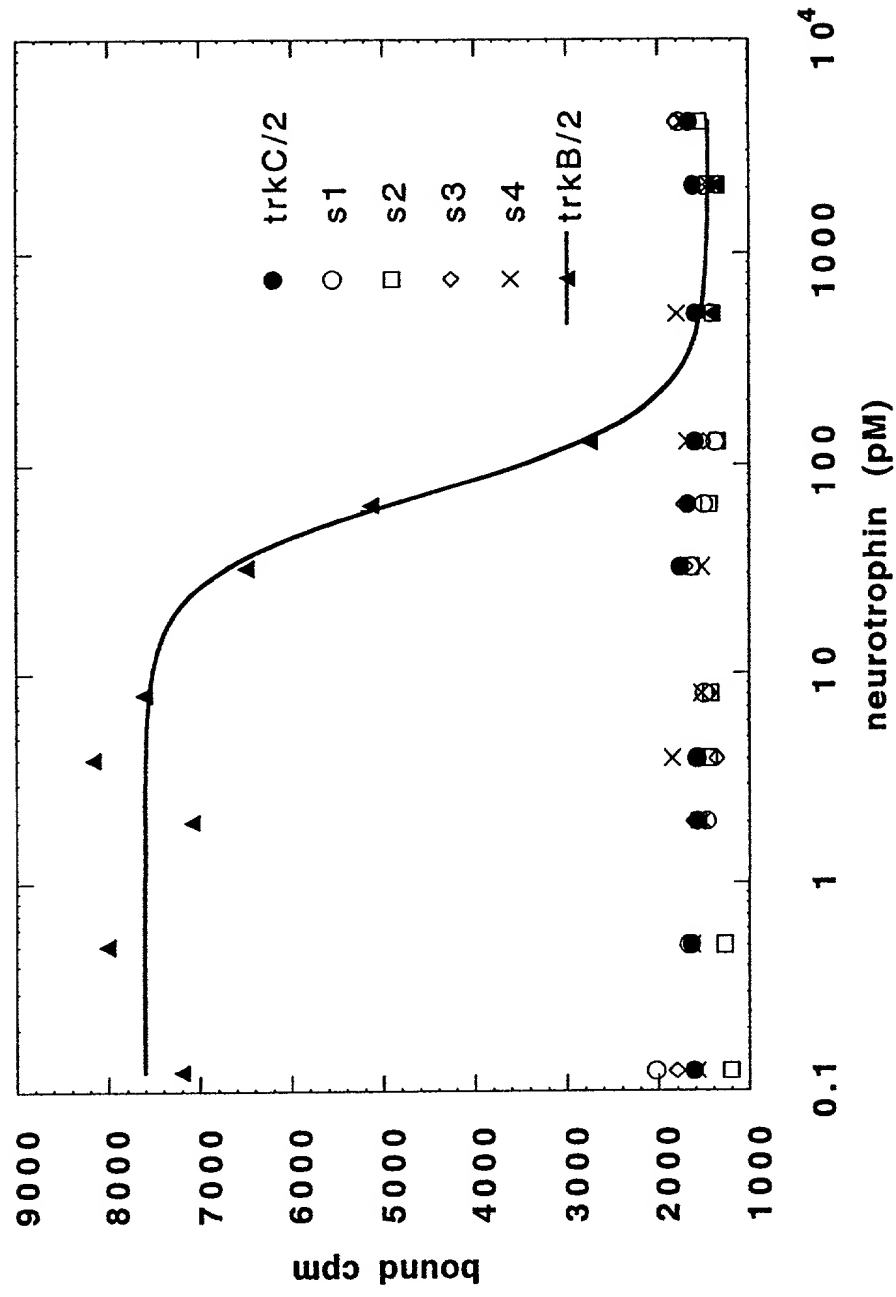


FIG. 15B

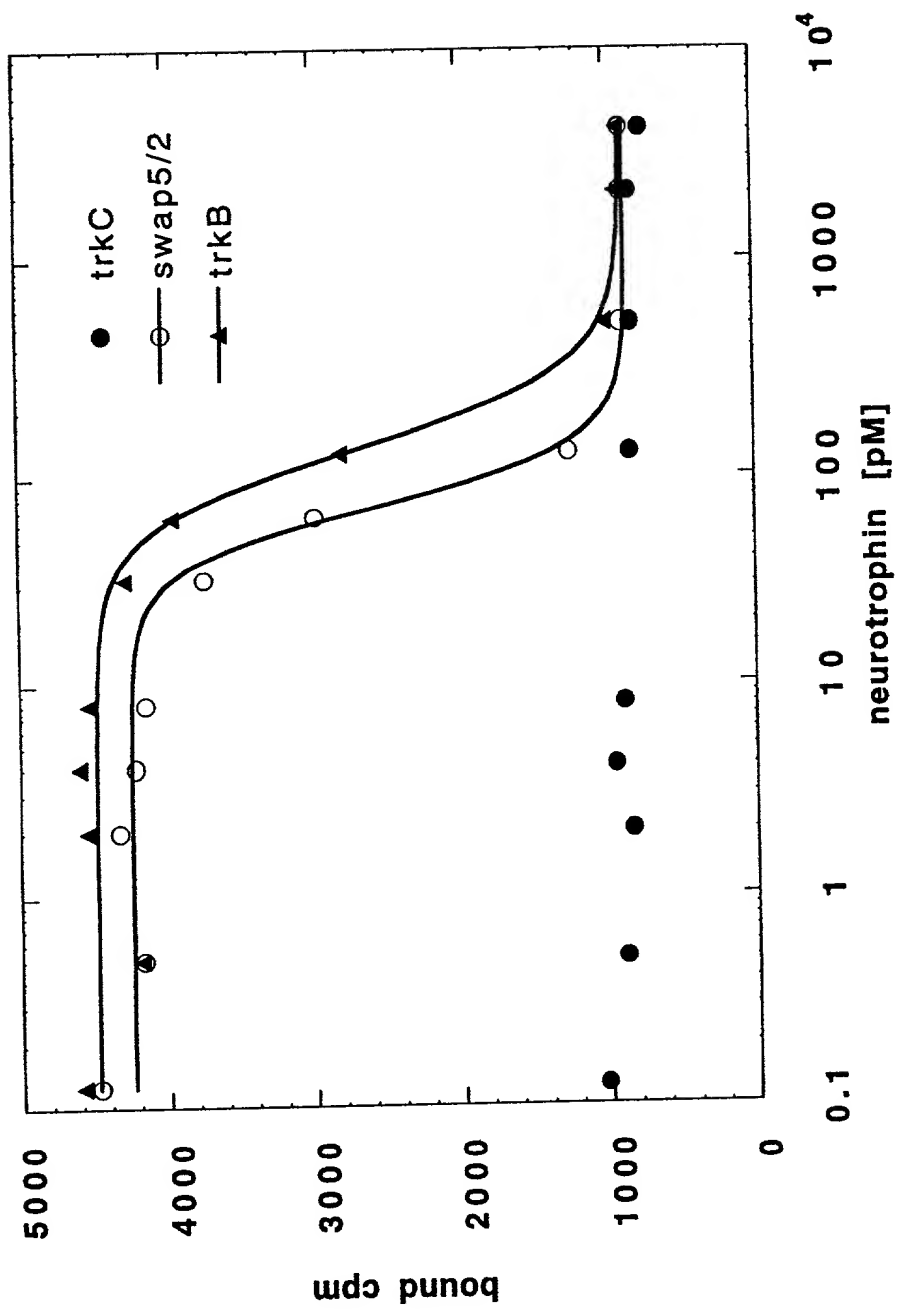


FIG. 15C

<i>trkA</i>	1	MLRGRRGQLGWHSWAAGPSSLAWLILAS	Signal	AGAAPCPDACCP
<i>trkB</i>	1	-----MSSWIRWHGPAMARLWGFCWLVGFW		-----RAAFACPTS-CK
<i>trkC</i>	1	-----MDVSL		-----CPAKCSFWRI-FLGSVWLDYVGSVLACPAN-CV
			Cysteine Rich I	
		HGSSGLRCTR-DGALDSLHHLPG		-----AENLYELYIENQQ
		CSASRIWCSDPSPGIVAFPRLEPNSVD		-----PENITEIFIANKOK
		CSKTEINCRRPDDGNL-FPLLEGODSGNSNGNANINITDISRNITSIHIENWR		
			Leucine Rich	
<i>trkA</i>	78	HLQHLELRDLRGLGELRNLTIVKSGLRFVAPDAFHFTPRLSRLNLSF		
<i>trkB</i>	78	RLEIINEDDVEAYVGLRNLTIVDSGLKFFVAHKAFKNSNLQHINFTR		
<i>trkC</i>	90	SLHTLNAVDMELYTGLOKLYIKNSGLRSIQPRAFAKNPHLRYINLSS		
			Cysteine Rich II	
		NALESLSWKTVQGLSLQELVLSGNPLHCSICALRWLQRWEEEGLGGVPEOKLQC		
		NKLTSLSRKHFRHLDLSELILVGNPFCTCSCDIHWIKTLQE-AKSSPDITQDLYC		
		NRLTTLWOLFOTLSLRELQLEONFFNCSCDIRWMOLWQEGEAKLNSONLYC		
<i>trkA</i>	178	HGQG		-----PLAHMPNASCGVPTLKVOVPNASVDVGDVLLRCQVEGR
<i>trkB</i>	177	LNESSKNIPLANLOIPNCGLPSPANLAAAPNLTVEEGKSIITLSCSVAGD		
<i>trkC</i>	190	INADGSOLPLFRMNI SQCDLPEISVSHVNLTVREGDNNAVITCNGSGS		
			Immunoglobulin I	
		GLEQAGWILTELEQSAIVMKS		-----GGLPSLGLTLANVITSDLNRKNLTCWAEND
		PVPNMVWDVGNLVSKHMET		-----SHTQG-SLRITNISSDDSGKQISCV AENL
		PLPDVDWIVTGLQOSINTHOTNLNWTNVTYHAINLTLYNVITSEDN GFTLTICIAENV		

FIG. 16A

<i>trkA</i>	271	VGRAEVSVQVNVSFPA	SVQ - LHTAVEMHHWC	IPFSVDGOPAPSLRWL
<i>trkB</i>	272	VGEDODSVNLT	VHFAPTIITFLESPTSDHHWC	IPFTVKGPKPALQWF
<i>trkC</i>	290	VGMSNASVALTV	YYP	PRVVSLEELRLEHCIEFVVRGNPPPTLHWL
		<hr/> Immunoglobulin II <hr/>		
		FNGSVLNETSFI	TFLEPAANETVRHGCLRLN	QPTHVNNGNYYTLAANPFGQ
		YNGAILNESKYI	CTKIH - - VINHTEYHGCLQL	DNPTTHMNNMGDYTLIAKNEYGK
		HNGOPLRESKI	IHV EY - - QEGEIS - EGCLLFN	KPTHYNNGNYYTLIAKNPLGT
<i>trkA</i>	370	ASASIMAAF	M - - - - - DNP	F - - - - - EF - NPEDPIPDINS - - - -
<i>trkB</i>	370	DEKOISAHFM	GWPGIDDGANPNYP	VDVIYEDYGTAAANDIGDITNRSNE
<i>trkC</i>	387	ANQTINGHFL	- - - - -	KEPFPEST - DNFIILFDEVST - - - - -
		<hr/> Transmembrane <hr/>		
		- TSGDPVEKKDEI	- - - PFGVSVAVGLAV	GFACLFSLTLLVLNKCGRRNKFGIN
		IPSTDVTDKTGR	EHL	SVYAVVVIASVVGFC - LLVMLFLL - - KLARHSKFGMK
		- PPITVTHKPEED	- - - TFGVSI	AVGLAAAFACVLLVLFVMI
		<hr/> Juxtamembrane <hr/>		
<i>trkA</i>	446	RP - AVLAP	EDGLAMSLHFMTLGGSSLS	PTIE - GKGSGLQG - - - - HIIE
<i>trkB</i>	466	GPASV	ISNDSDSASPLHHIS	NGSNTPSSSEGGPD
<i>trkC</i>	466	GPVAV	ISGGEEDSASPLHHI	NHGIIITPSSLDAGPDTVVIGMTIPVIE
		<hr/>		
		NPOYF - - - - -	SDACVHHIKRRDI	VLKWEELGEGAFGKVFLAECHNLLPEOD
		NPOYFGITNSOL	KPDTFVQH	IKRRHNI
		NPOYFR	OGHNCHK	PPDTYVQH
				IKRRDI
				VLKREL
				GEGAFGKVFLAE
				CYNL
				SP
				TKD

FIG. 16B

<i>trkA</i>	532	KMLVAVKALKEASESARQDFOREAEELLTMOHQHIVRFFGVCTEGRP
<i>trkB</i>	566	XILVAVKTLKDA SDNARKDFHREAEELLTNLOHEHIVKFFYGVCVEGDP
<i>trkC</i>	566	XMLVAVKALKDPTLAARKDFOREAEELLTNLOHEHIVKFFYGVCVGDDP
		Tyrosine Kinase
		LLMVFEYMRHGDNLNRF LRSHGPD AKLLAGGEDV - APGPLGLGQLLAVASQVAA
		LIMVFEYMKHGDNLNKF LRAHGPD AVLMAEGNPP - - TELTQSOMLHIAQQIAA
		LIMVFEYMKHGDNLNKF LRAHGPD AMILVDGGQPROAKGELGLSQMLHIASOIAS
<i>trkA</i>	631	GMVYLAGLHFVHRDLATRNCLVGGGLVVKIGDFGMSRDIYSTDYR -
<i>trkB</i>	663	GMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDIYSTDYR -
<i>trkC</i>	666	GMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDIYSTDYRL
		-----VGGRTMLPIRWMPPESILYRKFTTESDVWSFGVVLWEIFT
		-----VGGHTMLPIRWMPPESIMYRKFTTESDVWSLGVVLWEIFT
		FNPSGNDFCIMCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFT
<i>trkA</i>	717	YGKQPWYQLSNTAEIDCITQGRELERPRACPPPEVYAIMRGCWOREPO
<i>trkB</i>	749	YGKQPWYQLSNNEVIECITQGRVLRPRPTCPOEVYELMLGCWOREPH
<i>trkC</i>	766	YGKQPWFOLSNTIEVIECITQGRVLERPRVCPKEVYDVMLGCWOREPO
		QRHSIKD V HARLQALAOAPPVYLDVLG
		MRKNIKGIHTLLONLAKASPVYLDILG
		ORLNIKEIYKILHALGKATPIYLDILG

FIG. 16C

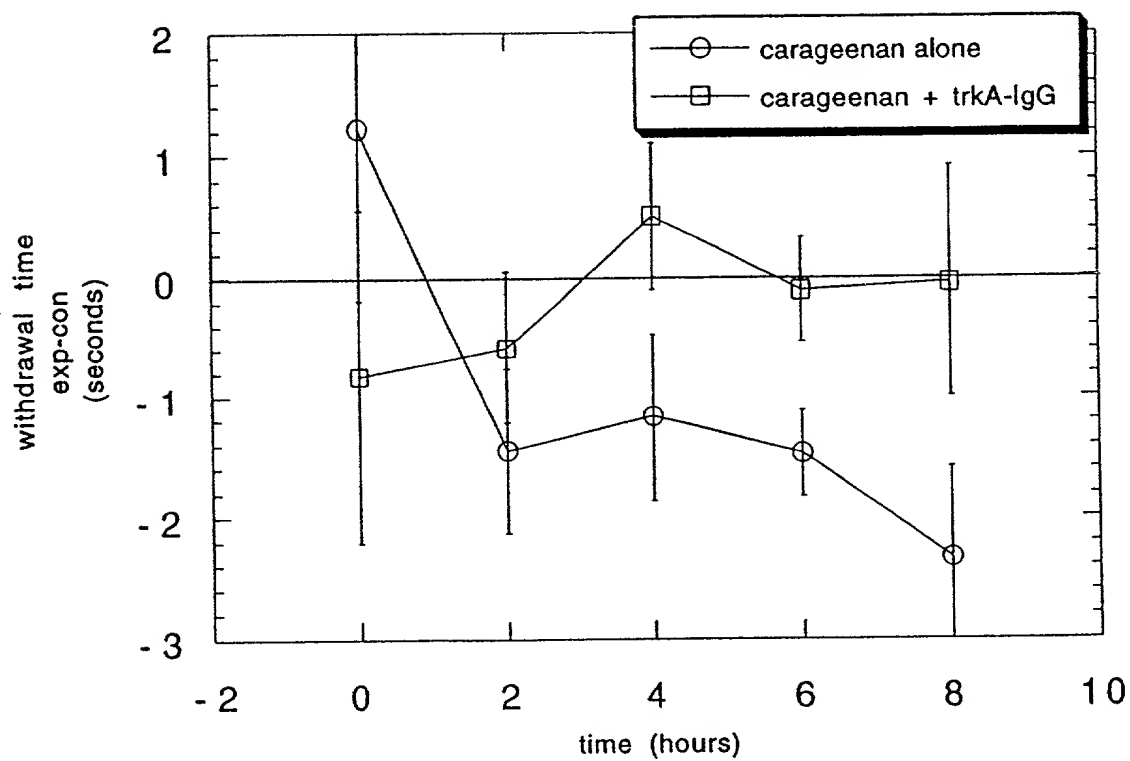


FIG. 17

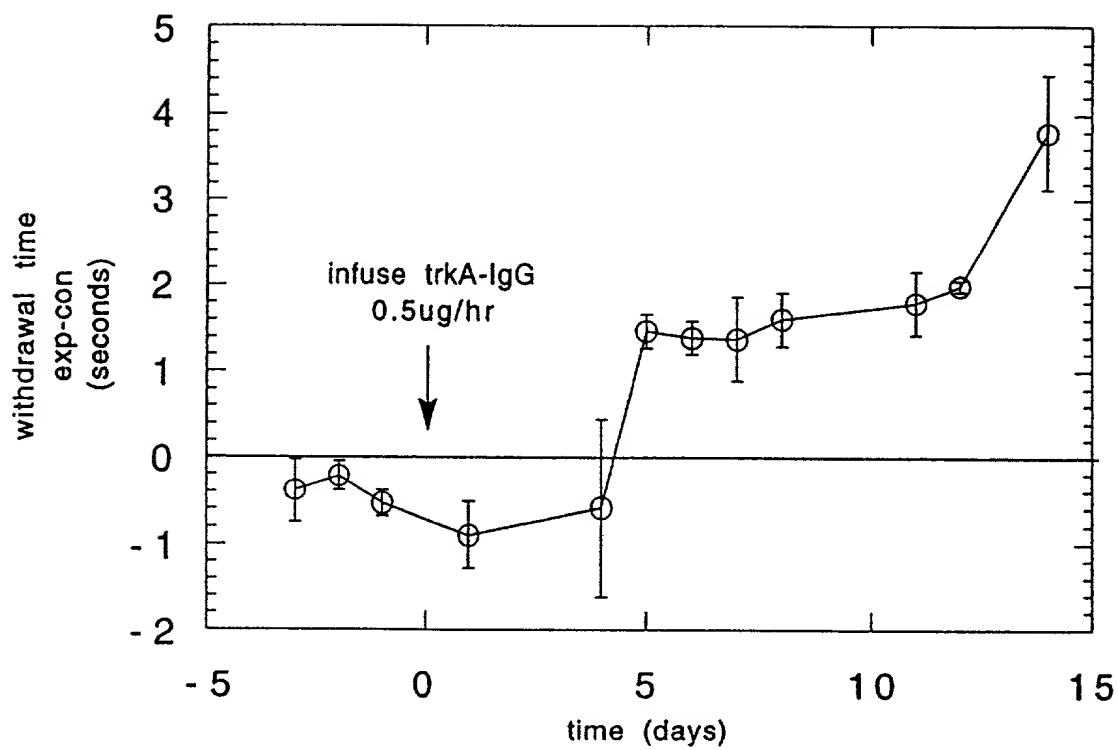


FIG. 18